

SEQUENCE LISTING

(1) GENERAL INFORMATION:



- (i) APPLICANT: Ceriani, Roberto L.
Peterson, Jerry A.
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON HMFG
DIFFERENTIATION ANTIGEN BINDING
SPECIFICITY, COMPOSITION, KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: V. Amzel & Assoc.
(B) STREET: P.O.Box 159
(C) CITY: Gladwyne
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19035
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk 3.5"
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
(D) SOFTWARE: PatentIn #1.0,
Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/482,596
(B) FILING DATE: June 7, 1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Amzel, Viviana
(B) REGISTRATION No.: 30,930
(C) REFERENCE/DOCKET No.: CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-649-0609
(B) TELEFAX: 240-359-0299
(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTTTCATCC	ATGATGTTAA	TAAAAAACAC	AAGGAGTTTG	TGGGTAAC TG	50
GAACAAAAAC	GCGGTGCATG	TCAACCTGTT	TGAGACCCCT	GTGGAGGCTC	100
AGTACGTGAG	ATTGTACCCC	ACGAGCTGCC	ACACGGCCTG	CACTCTGCGC	150
TTTGAGCTAC	TGGGCTGTGA	GCTGAACGGA	TGCGCCAATC	CCCTGGGCCT	200

GAAGAATAAC	AGCATCCCTG	ACAAGCAGAT	CACGGCCTCC	AGCAGCTACA	250
AGACCTGGGG	CTTGCATCTC	TTCAGCTGGA	ACCCCTCCTA	TGCACGGCTG	300
GACAAGCAGG	GCAACTTCAA	CGCCTGGGTT	GCGGGGAGCT	ACGGTAACGA	350
TCAGTGGCTG	CAGGTGGACC	TGGGCTCCTC	GAAGGAGGTG	ACAGGCATCA	400
TCACCCAGGG	GGCCCGTAAC	TTTGGCTCTG	TCCAGTTTGT	GGCATCCTAC	450
AAGGTTGCCT	ACAGTAATGA	CAGTGCGAAC	TGGACTGAGT	ACCAGGACCC	500
CAGGACTGGC	AGCAGTAAGA	TCTTCCCTGG	CAACTGGGAC	AACCACTCCC	550
ACAAGAAGAA	CTTGTTTGAG	ACGCCCATCC	TGGCTCGCTA	TGTGCGCATC	600
CTGCCTGTAG	CCTGGCACAA	CCGCATCGCC	CTGCGCCTGG	AGCTGCTGGG	650
CTGTTAGTGG	CCACCTGCCA	CCCCCAGGTC	TTCCTGCTTT	CCATGGGCCC	700
GCTGCCTCTT	GGCTTCTCAG	CCCCTTTAAA	TCACCATAGG	GCTGGGGACT	750
GGGGAAGGGG	AGGGTGTTC	GAGGCAGCAC	CACCACACAG	TCACCCCTCC	800
CTCCCTCTTT	CCCACCTCC	ACCTCTCACG	GGCCCTGCCC	CAGCCCCTAA	850
GCCCCGTCCC	CTAACCCCCA	GTCTCACTG	TCCTGTTTTT	TTAGGCACTG	900
AGGGATCTGA	GTAGGTCTGG	GATGGACAGG	AAAGGGCAAA	GTAGGGCGTG	950
TGGTTTCCCT	GCCCCTGTCC	GGACCGCCGA	TCCCAGGTGC	GTGTGTCTCT	1000
GTCTCTCCTA	GCCCCTCTCT	CACACATCAC	ATTCCCATGG	TGGCCTCAAG	1050
AAAGGCCCCG	AAGCCCCAGG	CTGGAGATAA	CAGCCTCTTG	CCCGTCGGCC	1100
CTGCGTCGGC	CCTGGGGTAC	CATGTGCCAC	AACTGCTGTG	GCCCCCTGTC	1150
CCCAAGACAC	TTCCCCTTGT	CTCCCTGGTT	GCCTCTCTTG	CCCCTTGTCC	1200
TGAAGCCCAG	CGACACAGAA	GGGGGTGGGG	CGGGTCTATG	GGGAGAAAGG	1250
GAGCGAGGTC	AGAGGAGGGC	ATGGGTGGGC	AGGGTGGGCG	TTTGGGGCCC	1300
TCATGCTGGC	TTTTTACCCC	AGAGGACACA	GGCAGCTTCC	AAAATATATT	1350
TATCTTCTTC	ACGGGAAAAA	AAAAAAAAAA	ACCG		1384

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp	Phe	Ile	His	Asp	Val	Asn	Lys	Lys	His	Lys	Glu	Phe	Val
1				5					10				
Gly	Asn	Trp	Asn	Lys	Asn	Ala	Val	His	Val	Asn	Leu	Phe	Glu
15					20					25			
Thr	Pro	Val	Glu	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Thr	Ser
						35					40		
Cys	His	Thr	Ala	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys
							50					55	
Glu	Leu	Asn	Gly	Cys	Ala	Asn	Pro	Leu	Gly	Leu	Lys	Asn	Asn
									65				70
Ser	Ile	Pro	Asp	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Ser	Tyr	Lys
									80				
Thr	Trp	Gly	Leu	His	Leu	Phe	Ser	Trp	Asn	Pro	Ser	Tyr	Ala
										95			
Arg	Leu	Asp	Lys	Gln	Gly	Asn	Phe	Asn	Ala	Trp	Val	Ala	Gly
											110		
Ser	Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser
												125	
Ser	Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn
													140
Phe	Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr
Ser	Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg
Thr	Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His
Ser	His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg
Tyr	Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala
				200				205					210

Leu Arg Leu Glu Leu Leu Gly Cys
215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe	Ile	His	Asp	Val	Asn	Lys	Lys	His	Lys	Glu	Phe	Val	Gly
1				5					10				
Asn	Trp	Asn	Lys	Asn	Ala	Val	His	Val	Asn	Leu	Phe	Glu	Thr
15				20					25				
Pro	Val	Glu	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Thr	Ser	Cys
30				35					40				
His	Thr	Ala	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu
		45				50						55	
Leu	Asn	Gly	Cys	Ala	Asn	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Ser
		60						65					70
Ile	Pro	Asp	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Ser	Tyr	Lys	Thr
		75						80					
Trp	Gly	Leu	His	Leu	Phe	Ser	Trp	Asn	Pro	Ser	Tyr	Ala	Arg
85				90					95				
Leu	Asp	Lys	Gln	Gly	Asn	Phe	Asn	Ala	Trp	Val	Ala	Gly	Ser
100				105						110			
Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser	Ser
		115				120					120		
Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn	Phe
		130						135					140
Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr	Ser
		145						150					
Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg	Thr
155				160					165				
Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His	Ser
170				175						180			
His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg	Tyr
		185				190					195		
Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala	Leu
		200					205						210
Arg	Leu	Glu	Leu	Leu	Gly	Cys							
			215		217								

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe	Lys	Gly	Asn	Ser	Thr	Arg	Asn	Val	Met	Tyr	Phe	Asn	Gly
1				5					10				
Asn	Ser	Asp	Ala	Ser	Thr	Ile	Lys	Glu	Asn	Gln	Phe	Asp	Pro
15				20					25				
Pro	Ile	Val	Ala	Arg	Tyr	Ile	Arg	Ile	Ser	Pro	Thr	Arg	Ala
30				35					40				
Tyr	Asn	Arg	Pro	Thr	Leu	Arg	Leu	Glu	Leu	Gln	Gly	Cys	Glu
		45				50						55	
Val	Asn	Gly	Cys	Ser	Thr	Pro	Leu	Gly	Met	Glu	Asn	Gly	Lys
		60						65					70
Ile	Glu	Asn	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Phe	Lys	Lys	Ser
		75						80					
Trp	Trp	Gly	Asp	Tyr	Trp	Glu	Pro	Phe	Arg	Ala	Arg	Leu	Asn

85					90					95				
Ala	Gln	Gly	Arg	Val	Asn	Ala	Trp	Gln	Ala	Lys	Ala	Asn	Asn	
100					105					110				
Asn	Lys	Gln	Trp	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Ile	Lys	Lys	
	115						120					125		
Ile	Thr	Ala	Ile	Ile	Thr	Gln	Gly	Cys	Lys	Ser	Leu	Ser	Ser	
	130							135				140		
Glu	Met	Tyr	Val	Lys	Ser	Tyr	Thr	Ile	His	Tyr	Ser	Glu	Gln	
			145					150						
Gly	Val	Glu	Trp	Lys	Pro	Tyr	Arg	Leu	Lys	Ser	Ser	Met	Val	
155					160					165				
Asp	Lys	Ile	Phe	Glu	Gly	Asn	Thr	Asn	Thr	Lys	Gly	His	Val	
170					175					180				
Lys	Asn	Phe	Phe	Asn	Pro	Pro	Ile	Ile	Ser	Arg	Phe	Ile	Arg	
	185						190					195		
Val	Ile	Pro	Lys	Thr	Trp	Asn	Gln	Ser	Ile	Ala	Leu	Arg	Leu	
		200						205					210	
Glu	Leu	Phe	Gly	Cys	Asp	Ile	Tyr							
				215			218							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly
1				5					10				
Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro
15					20				25				
Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr
	30					35					40		
Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp
	45					50					55		
Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala
	60						65					70	
Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn
	75							80					
Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
85					90				95				
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro
100					105				110				
Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val
	115						120				125		
Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Glu
	130						135					140	
Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly
			145					150					
His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val
155					160				165				
Phe	Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser
170					175					180			
Leu	Asp	Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro
	185						190					195	
Gln	Ser	Trp	Val	His	Gln	Ile	Ala	Leu	Arg	Met	Glu	Val	Leu
	200						205					210	
Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr						
					215		218						